S03196-00-US

Replacement Sheet

line numbers edited throughout to establish total number of pages

Figures

Figure 1 - Nucleotide and protein sequence of Aspergillus ochraceus 11

alpha hydroxylase

```
5     tggaagtttt tacacttatt atgccggagc cgaaagattc tgagtcgagg ggttgggggaa    60
      caacactata agacctacaa ccacttggat ttggtgaatt tacacgggca ttatcaaaac   120
      agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg   172
                                  Met Pro Phe Phe Thr Gly Leu Leu Ala
                                   1                   5

10    att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc   220
      Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr
       10              15                  20                  25

15    att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc   268
      Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser
                          30              35                  40

      gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt   316
20    Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg
                      45              50                  55

      cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg   364
25    Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg
                  60                  65                  70

      ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg   412
      Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp
           75                  80                  85
30
      gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac   460
      Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn
       90                  95                  100                 105

35    gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga   508
      Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly
                          110                 115                 120

      tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa   556
40    Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys
                      125                 130                 135

      gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg   604
      Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro
45                140                 145                 150

      atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat   652
      Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp
           155                 160                 165
50
      cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc   700
      Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val
      170                 175                 180                 185

55    gcc cgg atg tcg aca aga gtg ttc ctt ggc gag gaa atg tgc aat aac   748
      Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn
                          190                 195                 200

      cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt   796
60    Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly
                      205                 210                 215

      gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta   844
      Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val
65                220                 225                 230

      cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc   892
      His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Arg Ser Leu Arg Arg
           235                 240                 245
70
      tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag   940
      Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys
      250                 255                 260                 265
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Replacement Sheet

insert ← "Figure 1, continued"

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        ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc    988
        Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile
                     270             275                 280
 5
        gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag   1036
        Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys
                     285                 290             295
10
        cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc   1084
        Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu
                     300             305                 310
15
        ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca   1132
        Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala
                 315             320                 325
20
        gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag   1180
        Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys
        330                 335                 340             345
25
        gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc   1228
        Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser
                     350             355                 360

        cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg   1276
        Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr
                     365             370                 375
30
        aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga   1324
        Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg
                     380             385                 390
35
        gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac   1372
        Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp
                395             400                 405

        cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc   1420
        Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro
        410             415                 420                 425
40
        ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg   1468
        Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met
                     430             435                 440
45
        gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc   1516
        Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser
                     445             450                 455
50
        aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg   1564
        Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp
                     460             465                 470
55
        cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act   1612
        Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr
             475             480                 485

        tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg   1660
        Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala
        490                 495                 500                 505
60
        gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat     1710
        Glu Ile Asp Met Ala Ser Leu Thr Val  *
                     510
65
        gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat 1770
        aaaaaa                                                           1776
```

line numbers changed to address additional lines originally on page 1 of 25.

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Figure 2 - Nucleotide and protein sequence of human
oxidoreductase

```
5        atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg      48
         Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val
         1               5                   10                  15

10       gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg      96
         Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
                         20                  25                  30

         ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa     144
         Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
15                       35                  40                  45

         gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc     192
         Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
20                       50                  55                  60

         aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc     240
         Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
         65                  70                  75                  80

25       atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac     288
         Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
                             85                  90                  95

30       cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg     336
         Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
                         100                 105                 110

         gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc     384
         Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
35                       115                 120                 125

         gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac     432
         Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
                         130                 135                 140

40       ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac     480
         Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp
         145                 150                 155                 160

45       gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag     528
         Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys
                             165                 170                 175

         acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg     576
         Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu
50                       180                 185                 190

         gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac     624
         Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp
55                       195                 200                 205

         gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg     672
         Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp
         .   210            ·            215                 220

60       ccg gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc     720
         Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser
         225                 230                 235                 240

65       agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc     768
         Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala
                             245                 250                 255

         aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag     816
         Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln
70                       260                 265                 270

75       aag ccc ccc ttt gat gcc aag aat ccg ttc ctg gct gca gtc acc acc     864
         Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr
                         275                 280                 285

         aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa     912
```

```
      Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu
          290             295             300

 5    ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg    960
      Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val
      305             310             315             320

      gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg ggc aaa   1008
10    Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys
                      325             330             335

      atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat   1056
      Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp
15                    340             345             350

      gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc   1104
      Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg
                      355             360             365

20    acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac   1152.
      Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn
                      370             375             380

      gtg ctg tac gag ctg gcg cag tac gcc tcg gag ccc tcg gag cag gag   1200
25    Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu
      385             390             395             400

      ctg ctg cgc aag atg gcc tcc tcc tcc ggc gag ggc aag gag ctg tac   1248
      Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr
30                    405             410             415

      ctg agc tgg gtg gtg gag gcc cgg agg cac atc ctg gcc atc ctg cag   1296
      Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln
                      420             425             430
35
      gac tgc ccg tcc ctg cgg ccc ccc atc gac cac ctg tgt gag ctg ctg   1344
      Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu
                      435             440             445

40    ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc   1392
      Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val
          450             455             460

      cac ccc aac tct gtg cac atc tgt gcg gtg gtt gtg gag tac gag acc   1440
45    His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr
      465             470             475             480

      aag gcc ggc cgc atc aac aag ggc gtg gcc acc aac tgg ctg cgg gcc   1488
      Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala
50                    485             490             495

      aag gag cct gcc ggg gag aac ggc ggc cgt gcg ctg gtg ccc atg ttc   1536
      Lys Glu Pro Ala Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe
                      500             505             510
55
      gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc acg cct gtc   1584
      Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val
          515             520             525

60    atc atg gtg ggc ccc ggc acc ggg gtg gca ccc ttc ata ggc ttc atc   1632
      Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile
      530             535             540

      cag gag cgg gcc tgg ctg cga cag cag ggc aag gag gtg ggg gag acg   1680
65    Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr
      545             550             555             560

      ctg ctg tac tac ggc tgc cgc cgc tcg gat gag gac tac ctg tac cgg   1728
      Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg
70                    565             570             575

      gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac   1776
      Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
75                    580             585             590

      gtg gcc ttc tcc cgg gag cag tcc cac aag gtc tac gtc cag cac ctg   1824
      Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
                      595             600             605

80    cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa ggc ggt gcc   1872
      Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
```

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Replacement Sheet

← Insert

"Figure 2, Continued"

```
           610                615                620
 5    cac atc tac gtc tgt ggg gat gca cgg aac atg gcc agg gat gtg cag     1920
      His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
      625                 630                635                640

10    aac acc ttc tac gac atc gtg gct gag ctc ggg gcc atg gag cac gcg     1968
      Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
                  645                650                655

      cag gcg gtg gac tac atc aag aaa ctg atg acc aag ggc cgc tac tcc     2016
      Gln Ala Val Asp Tyr Ile Lys Lys Leu Met Thr Lys Gly Arg Tyr Ser
                  660                665                670

15    ctg gac gtg tgg agc                                                 2031
      Leu Asp Val Trp Ser
                  675
```

Figure 3 - Nucleotide and protein sequence of *Aspergillus* *ochraceus oxidoreductase*

```
 5      cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttcct      60
        cttctgactc ccttttttgtt attgatcgcc catctcggtg aacatttggg atatctttcc     120
        ctctcccccct cccgccccga ccctccttat cttctcctcc cgtccagcat ttagctcgcc     180
        atcgaattcg caattccttc ctcgtgactc ttcatcgctg agcgtcctca tc atg gcg      238
                                                                 Met Ala
                                                                  1

10      caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt        286
        Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly
                  5                   10                  15

15      agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac        334
        Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp
                20                  25                  30

        cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc ggc        382
20      Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly
        35                  40                  45                  50

        aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt        430
25      Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys
                        55                  60                  65

        gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc        478
        Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser
30                      70                  75                  80

        aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg        526
        Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val
                    85                  90                  95

35      gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag        574
        Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu
                100                 105                 110

        gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc        622
40      Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro
        115                 120                 125                 130

        acg gat aat gcg gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct        670
45      Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala
                        135                 140                 145

        gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc        718
        Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu
50                      150                 155                 160

        aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac        766
        Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn
                    165                 170                 175

55      gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa        814
        Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln
                180                 185                 190

        cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa        862
60      Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu
        195                 200                 205                 210

        gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag        910
65      Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu
                        215                 220                 225

        gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat        958
        Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn
                        230                 235                 240

70      gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc       1006
        Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu
                    245                 250                 255

75      ggt gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac       1054
        Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr
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"Figure 3, continued"

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              260                 265                 270
      tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg    1102
 5    Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu
      275                 280                 285                 290

      ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc    1150
      Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala
10                        295                 300                 305

      ggt agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc    1198
      Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro
                          310                 315                 320

15    acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc    1246
      Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu
                          325                 330                 335

      gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc    1294
20    Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr
                          340                 345                 350

      gct aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc    1342
      Ala Lys Val Pro Ile Pro Thr Pro Thr Thr Tyr Asp Ala Ala Val Arg
25    355                 360                 365                 370

      tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tcg act    1390
      Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr
                          375                 380                 385
30
      ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt    1438
      Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg
                          390                 395                 400

35    ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc    1486
      Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys
                          405                 410                 415

      ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc    1534
40    Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr
                          420                 425                 430

      gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc    1582
45    Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro
      435                 440                 445                 450

      cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att    1630
      Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile
                          455                 460                 465
50
      agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac    1678
      Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His
                          470                 475                 480

55    att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag    1726
      Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys
                          485                 490                 495

      caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc    1774
60    Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile
                          500                 505                 510

      act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc    1822
65    Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val
      515                 520                 525                 530

      cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc    1870
      Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile
                          535                 540                 545
70
      atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag    1918
      Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln
                          550                 555                 560

75    gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg    1966
      Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu
                          565                 570                 575

      ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat    2014
80    Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp
                          580                 585                 590
```

```
      gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc    2062
      Glu Trp Lys Thr Phe Gln Glu Gln Leu Gly Asp Ser Leu Lys Ile Ile
5     595                 600             605                 610

      act gcc ttc tct cgt gaa tcg gct gag aaa gtc tac gtc cag cac agg    2110
      Thr Ala Phe Ser Arg Glu Ser Ala Glu Lys Val Tyr Val Gln His Arg
                      615             620                 625

10    ctg cgt gag cat gcc gag ctg gtc agt gac ctg ctg aag cag aaa gcc    2158
      Leu Arg Glu His Ala Glu Leu Val Ser Asp Leu Leu Lys Gln Lys Ala
                      630             635                 640

      act ttc tat gtt tgc ggt gac gct gcc aac atg gcc cgt gaa gtc aac    2206
15    Thr Phe Tyr Val Cys Gly Asp Ala Ala Asn Met Ala Arg Glu Val Asn
                  645             650             655

      ctc gtg ctt ggg caa atc att gcc aag cag cgc ggt ctc cct gcc gag    2254
      Leu Val Leu Gly Gln Ile Ile Ala Lys Gln Arg Gly Leu Pro Ala Glu
20                660             665             670

      aag ggc gag gag atg gtg aag cac atg cgc agc agc ggc agc tac cag    2302
      Lys Gly Glu Glu Met Val Lys His Met Arg Ser Ser Gly Ser Tyr Gln
      675                 680                 685                 690
25
      gac gat gtc tgg tcc taa aa                                         2322
      Asp Asp Val Trp Ser  *
                      695
```

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Figure 4 - Amino acid homology alignment of A. ochraceus 11 alpha hydroxylase with the top 10 BLAST hits from GenBank

```
CAA75565    1 ---MANHSSSYYHEFYKDHSHTVLQLMSEKPVILPSLILGTCAVLLCIQWLK--PQPLIM
CAB91316    1 ---------------MERLDIKSIQDPSATPFSYLVTAFLLAVVVQSLQGPRF-PKNIKH
CAB56503    1 ------------------------------LLFCFILSKTTKKFGQNSQYS-NHDELP
AAB94588    1 -------------MVMELHNHTPFSIYFITSILFIFFVFFKLVQRS--DSKTS-STCKLP
pMON45624   1 ------------MPFFTGLLAIYHSLILDNPVQTLSTIVVLAAAYA-LATLQ--PSDLPE
CAA75566    1 ------------MSIFNMITSYAGSQLLPFYIAIFVFTLVPWAIRFSWLELRK-GSVVPL
AAD34552    1 ---MTVDALTQPHHLLSLAWNDTQQHGSWFAPLVTTSAGLLCLLIQLCSSGR--RSDLPV
CAA75567    1 ------------------------------------------------------------
CAA76703    1 MSKSNSMNSTSHETLFQQLVLGLDRMPLMDVHWLIYVAFGAWLCSHVIHVLSSSSTVKVP
CAA57874    1 ------------------------------------------------------------
CAA91268    1 ------------------MALLILSSLVISIFTFFIYIILARRERGKLREKIGLSGPEPH


CAA75565   56 VNGRKFGELSNVRAFRDFTFGARQLIEKGLKMSPDKPFRIMGDVGBIHILPFKYAYEVRN
CAB91316   45 LNFKGPLEFSDTPPRKEFVYGSPQMIANWFKANPNKPCRVISIFGEAIVLPERMANEIKN
CAB56503   28 PGFPQIPILGNAFQLSGGH-THHIURDLAKKYGPLMHLK-IGEVSTIVASSFQIABEIFR
AAB94588   45 PGFRTLPLIGNIFQIVGSLPVHYYLKNLADKYGPLMHLK-LGEVSNIIVTSFEMAQEIMK
pMON45624  46 LNFAKPFEFTNRFRVHEFVENSFSLIARGRELHGHEPYRLFSEWGSLVLILPFECADFLEN
CAA75566   48 ANFPD-SLFGTGFTRRSFVKLSREILAKFRSLFPNEPFRLWTDWGFVLIILPEDFADEIRN
AAD34552   56 FNFKTWWELTTMRAKRDFDANAPSWIESWFSQN-DKPIRFIVLSGYCTIILFSSMAEDFRK
CAA75567    1 ------------------------------------------------------------
CAA76703   61 VVGYRSVFEPTWLLFLRFVWEGGSIIGOGYNKFKDSIFQVRKLGTDIVIIPPNYIDEVRK
CAA57874    1 ------------------------------------------------------------
CAA91268   43 WFLGNLKQTAERKFRLGYDDANFWFNELHEQYGETFGIY-YGSQMNIVISNEKDIKEVFI


CAA75565  116 NEKLSFTMAA--FKWFYAHLPGFEG--FREGTNESHIKKLVARHQLT--HQLTLVTGAVS
CAB91316  105 DDRLSFTRWT--YKAFHGHLPGFEG--FGEASRESFIVQEVIMRDLT--RYLNKYTEPLA
CAB56503   86 THDILFADRPSNLESFKIVSYDFSDMVVSPYGNYWRQLRKISMMELLSQRSVQSFRSIRE
AAB94588  104 THDLNFSDRP-DFVLSRIVSYNGSGIVFSQHGDYWRQLRKICTVEILTAKRVQSFRSIRE
pMON45624 106 DPRLDFETPT--TDDSHGYIPGFDA-----LN-ADPNLTKVVTKYLT--KALNKLTAPLS
CAA75566  107 DPRLSFSKAA--MQDNHAGIPGFET--VALVGREDQLIQKVARKQLT--HHLSAVIEPLS
AAD34552  115 MKELCMYKFLG--TDFHSHLPGFDG--FKEVTRDAHLITKVVMNQFQ--TQAPKYVKPLA
CAA75567    1 ------------------------------------MKYTT--COMNIFPSLWS
CAA76703  121 LS----QDKTRSVEPFINDFAGQYT--RGMVFLQSDLQNRVIQQRLI--PKLVSITKVEK
CAA57874    1 ------------------------------------------------------------
CAA91268  102 KNFSNFSDRS--VPSIYEANQLTASLLMNSYSSGWNHTRSAIAPIFS-TGKFKAMQETTN


CAA75565  170 EECALVLKDMYTDSP--EWHDITAKDANMKLVARITSRVFLCKEMCRNPQWLRIT-STYA
CAB91316  159 QFTSMAFEANLPKAANGEWSTINIRSKILPIVARISSRVFLEEELCRNEWLKVI-QQYT
CAB56503  146 EEVLNFIKSIG---SKEG-TRINISKEISLLIYGILTRAAFCEKNKNTEEFIRLLDQLTK
AAB94588  163 EEVAELVKKIAATASEEGGSIFNLTQSHYSYTFGIAARAAFCKKSRYCQVEISNMHKQLM
pMON45624 156 HFASIAWKAVLGDDP--DWREIYPARDLLQLYARMSTRVFLCEEMCNNQDWIQTS-SQYA
CAA75566  161 RESTLAVSLNFGETT--EWRAIRIKPAILDILARISSRIYLFCDQLCRNEAWLKII-KTYT
AAD34552  169 NFASGIITDIFGDSN--EWHTVFVYNQCIDLVTRTVIFIMVGSKLAHNBEWLDIA-KHHA
CAA75567   17 MKTSFRWPRTS------KMSSVSIYDMMLRTWALLSGRAFVCLPLCRDEGWLQAS-IGVT
CAA76703  173 EELDYALTKEMPDMKNDEAVBVDISSIMVRLISRISARVFLGPEHCRNQBWLTTI-AEYS
CAA57874    1 ------------------------------------------------------------
CAA91268  159 SKVDLFLDILREKAS--SGQKWDIYDDFQGLTLDVIGKCAFRIDSNCQRDRNDVFYHPVT


CAA75565  227 VIAFRAVEELRLWF-SWLRPVVQWFMHCTQSRALVQEARDLINPLIER-RREEK---AEA
CAB91316  218 IDGFGAAEDLRLWF-AALRPIVHWFLBSCQRARADVRVARSILDFVLKK-RRQBK---AAN
CAB56503  202 AVAEPNIADEFPSL-KFLQLISTSKYKIEKIHKQFDVIVETILKGHKEYINZPLS--QEN
AAB94588  223 LLGGFSVADLYPSS-RVFQMAGATG-KLEKVHRVTDRVLQDLIDEHK---NRNRS--SEE
pMON45624 213 ALAFGVGDKLRIYF-RLIRPLVHWFMBSCWEERRSLRRCROILTFYIHS-RRSLK---GTT
CAA75566  218 TNFYTASTNLRMFF-RSLRPLAHWFLBECRKLRQERRDAIGLITPLIER-RRELR---RAA
AAD34552  226 VTMAIQARQLRLWF-VLLRPLVHWLEQGAKLRAQVRRARQLDPIIQE-RRABR---DAC
CAA75567   70 VQCVSIRDQLFTVS-PVLRPLIGPFIBSVRSVRRHLRFAABILAPLISQALQDEKQHRAD
CAA76703  232 ESLFITGFILRVVF-HILRFFIAPLIBSYRTLLRNVSSGRRVIGDLIIR----SQQ----
CAA57874    1 ----------MA-PMLRPLVYRFDIBERARIRDQWTKGRKRVMASNRE--RQBK--GGN
CAA91268  217 VKITINNFTYFHSSSPGTFHFLESTLQIHTTGRCRNSTCRRTVKCVGFRQDRAKFCSDYE
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(handwritten: "Replacement Sheet", "← insert", "Figure 4, continued")

```
       CAA75565  283  ERTGEKV-TYNDAVEALDDLAREK--EVGYDPACAQLSLSVAA--LHSTHDFFTQVMFDI
       CAB91316  274  ---GGKA-EHDDAIEAFERTA-K--CKYYDPAVAQLVLSIVA--IHTTSDLTCQVMTNL
       CAB56503  259  G--EKKE-DLVEVLLNIQRRNDFE--HPLGDKNIKAIIFNIFSAGTETSSTTVDWAMCEH
  5    AAB94588  276  R--EAVE-DLVEVLKFQKES--E--FRLTEDNIKAVIQDIFIGGGETSSSVVEWGMSEL
       pMON45624 269  DEQCKPL-MFDDSIEAFEREL---CPNHDAVLKQVTLSIVA--IHTTSDLILLQAMSDL
       CAA75566  274  IAACQPLPVFHDAIDWSEQEAEAAGTGASFDPVIFQLTLSIIA--IHTTYDLLQQTMIDL
       AAD34552  282  RAKCIEPPRYVDSIQAFEDTAK----CKWYDAAGAQLAPDFAG--IYGTSDLLIGGLVDI
       CAA75567  129  TLLGDQTEGRGTFISALLRHLP-EELRTPEQVGLDQMLVSFAA--IHTTIMALTKVVWEL
 10    CAA76703  282  ---CDGN---EDILSAMRDAATGEE-KQIDNIAQRMLILSIAS--IHTTAMTMTHAMYDL
       CAA57874   44  --LEDPPTMLDHLSNGRNEHIA----DDVELQLLHQKTLIAVE--TVTIFSSTTQRIYDL
       CAA91268  277  RRRGGEGSDSVELIKLLLNREDDKS-KPMTKQEVIBNCFSFLLAGYETTSTAMTYCSYLL


 15    CAA75565  338  AQNPELIEPLREEIIAVLGKQG------WSRNSLYNLRLMDSVLKESQRLK-E-------
       CAB91316  324  MQNPEFIAPLREEMIQVLSEGG------AKRTSLYNRLLDSVIKESQRVK-E-------
       CAB56503  314  IRNETVLKKAQEEVRKVFNEEGN-----VDETKLHQLKYLQAVIKETLRLH-E-------
       AAB94588  329  IRNERVMHEAQAEVRRVYDSKGY-----VDETELHQLIYLKSIIKETMRLH-E-------
       pMON45624 321  AQNEKVLCAVREEVVRVLSTEG------LSRVSLHSLRLMDSALKESQRLF-E-------
 20    CAA75566  332  GRHPEYIEPLRQEVVQLLREFG------AKRTTLFKZRLLDSAIKESQRMK-E-------
       AAD34552  336  VRHPHLLEPLRDEIRTVLGQGG------ATPASLYKLKLLDSCLKESQRVK-E-------
       CAA75567  186  VKRPEYIEPLFTELQDVFGPDAVSPDICINKERLSRLHKLDSFIREVQFWC-E-------
       CAA76703  333  CACPEYIEPLRDEVKSVLGASG------ADRTALNRFHKLDSFLKESQPFN-E-------
       CAA57874   96  VAHPEYITILREEVESVPRDPNGN---FIKDSTVANDKLDSFLKESQRFNSEDLSMSNL
 25    CAA91268  336  SKYENVQQKLYEDIMEAKENGG------LTYDSIHNMKYLLCVYKETLRFY-E-------


       CAA75565  384  ---------IAIASMRFFTTHNVKLSDCVILPKNKLTLVSAHQHW--------DPEYYKD
       CAB91316  370  ---------TGVASMRRYAEKDVTLSDGTFIPKGGFVAVSAHDMW--------NSEVYEQ
       CAB56503  361  ---------PVPLLLPRECREQCKIK-CYTIFSKSRVIVNAWAIGR-------DENYAIE
 30    AAB94588  376  ---------PVPLLLVPRVSRERCQIN-CYEIFSKTRIIINAWAIGR-------NPKYEGE
       pMON45624 367  ---------TLLGSFRFQATNDIKLKSGFVLKKGTPVVIDSTHHW--------NPEYYTL
       CAA75566  378  ---------GSIVTMRFYVTEDITLSSCLTFKKGTIVDNRRLD-------DEKIMDN
       AAD34552  382  ---------VECATMRSYALQDVTFSNGTFIPKGELVAVAPDRMS--------NPEVWPE
       CAA75567  238  ---------STFVIPSRRVMKSHTLSNCIKLQRGTSIAFFPAHAIHMSEETPTFSPLFSSE
 35    CAA76703  379  ---------VFLLIFNEIYHQSMTLSDCTNIFSGTRIAMPSHAKLQ-------DSAHVPG
       CAA57874  152  KNYKLCESLTGHSNLPTRTIADEKLPDGTFVPKGTKLEINTCSIHK-------DHKLAEN
       CAA91268  382  ---------PHFSFIRRLCREDITNIR-CQFYPKCAIVVCLFHTVHR-------NPENMDS


 40    CAA75565  427  ELK-----FDGYRFFNMFREP--GNESKAQLVSATPDHMGFGYCLHACPGRFFASBEIKI
       CAB91316  413  ABK-----WDGRRFLRMRETPGAGKENVAQLVSTAPBHLGFGHCQHACPGRFFAANEIKI
       CAB56503  404  PEK-----FNPDRFLES-------K---VDFKGNSFKYLPFGGGRFICPGITFALANIEL
       AAB94588  419  TES-----FKPERFLNS-------S---IDFRGIDFEFIPFGCARRICPCITFAIPNIEL
       pMON45624 410  ELQ-----YDGYRFFNKFQTP--GEDKNALLVSTSANHMGFGHCVHACPGRFFASNEIKI
 45    CAA75566  421  PEV-----YNFYRFYDMFSEA--GRDHGAQLVSTGSNHMGFGHCOHSCPGRFFAANEIKV
       AAD34552  425  BAK-----YDFYRYMRLFEDP--ANAFSAQLENTNGDHIGFGWHFRACPGRFFASKEIKV
       CAA75567  289  FENPSPRIFDGFRYLNLFSIK--CQGSQHQAATTGFDYLIFNHGHACPGRFFAISEIKI
       CAA76703  423  FTP--PTEFDGERYSKIFSDS--NYAQKYLFSMTDSSNMAFGYCYKYACPGRFYASNEMKI
       CAA57874  205  PEQ-----FDGLRFHKWRKAP--GNEKRYMYSSSGTEDLSAGFCFRHACPGRYLSAINIKL
 50    CAA91268  425  PRE-----EHPERFENWE------E------KSSSLKWIFGVGPRYCVGMRFAEMEFKT


       CAA75565  480  ALSHILLLKYDFRPV-----EGSSMEPRKYGLNGNANPTARLSVRRRK-EEIAI-----
       CAB91316  468  ALVHLLLLNYEWRLP-----EGSDPKIRTFCFSMGVDESLKVEYKGRQ-PEIEL-----
       CAB56503  449  PLAQLLFHFDWQS-----NTEKLNMKE-SRGVTVPREDDLYLTPVNFS-SSSPA-----
 55    AAB94588  464  PLAQLLYHEDWKLPNKMKNEELDMTE-SNGITLNRQNDLCLIPITR----LP------
       pMON45624 463  ALCHIILNYEWRLP-----DGFKPQPLNIGMTYLADENTRKLIRRRK-ABIDMASLTV
       CAA75566  474  ALCHILVKYDWKIC-----PDTETKPDTRGMIAKSSFVTDILIKRRESVELDLEAI--
       AAD34552  478  MLAYLLIRYDWKVV-----PDEPLQYYRHSFSVRIHETTKLMMRRRD-EDIRLPGSL-
 60    CAA75567  347  ILIPLLIAKYDFRIE-----DGKPGPELMRVGTETRLDTKAGLEMRRF----------
       CAA76703  479  TLAILLLQFEFRKLP---DGKGRPRNITIDSDLIPDFRARLCVRKRS---LRDE----
       CAA57874  258  IMABLLENYLIKLP-------DGLSRPKNIEFBVLASLNACANA--------------
       CAA91268  468  TIVKLIDTFELRQF----EGEADLIPDCNGVIMRPNDPVRLHLKFRN-----------


 65    CAA75565  (SEQ ID NO: 27)
       CAB91316  (SEQ ID NO: 28)
       CAB56503  (SEQ ID NO: 29)
       AAB94588  (SEQ ID NO: 30)
       pMON45624 (SEQ ID NO: 02)
 70    CAA75566  (SEQ ID NO: 31)
       AAD34552  (SEQ ID NO: 32)
       CAA75567  (SEQ ID NO: 33)
       CAA76703  (SEQ ID NO: 34)
       CAA57874  (SEQ ID NO: 35)
 75    CAA91268  (SEQ ID NO: 36)
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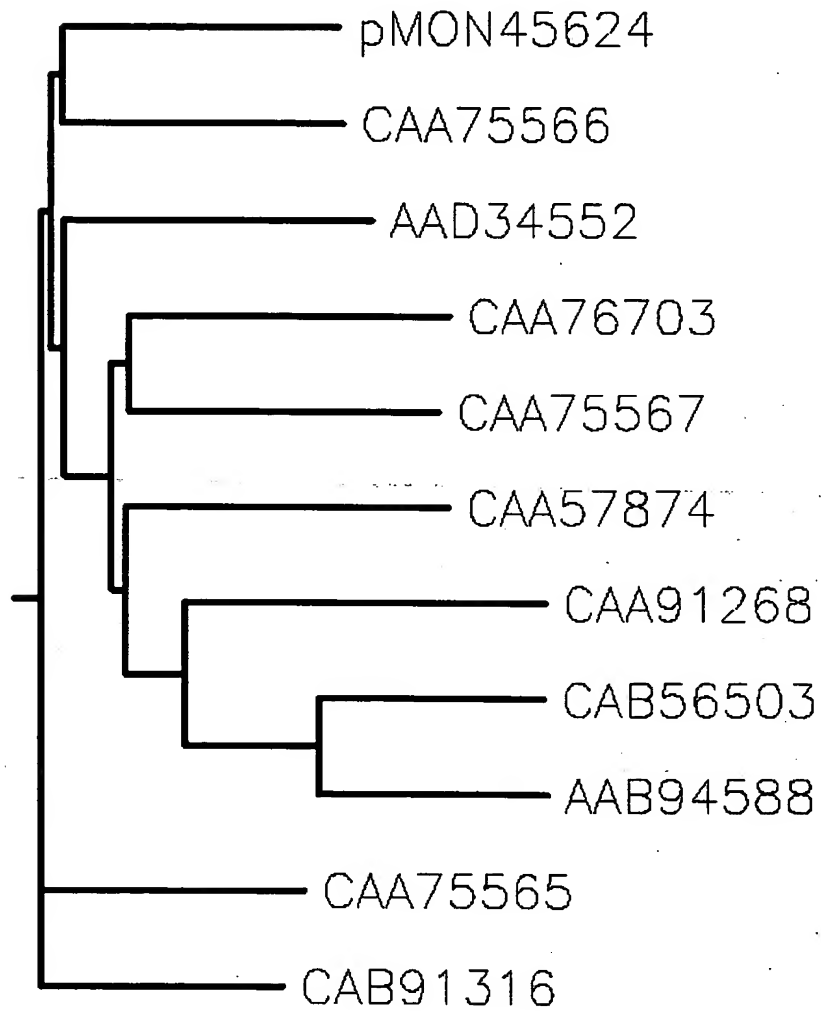
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**Figure 5 - Phylogenetic tree showing the relatedness of
Aspergillus ochraceus *11 alpha hydroxylase to the top 10*
BLAST hits from GenBank**

Figure 6 – Percent homology of Aspergillus ochraceus 11 alpha hydroxylase to the top 10 BLAST hits from GenBank

Accession Number	Species	% ID to 11a OH
CAB91316	*Neurospora crassa*	40
CAA76565	*Gibberella fujikuroi*	37
CAA75566	*Gibberella fujikuroi*	37
AAD34552	*Aspergillus terreus]*	29
CAA75567	*Gibberella fujikuroi*	24
CAA57874	*Fusarium oxysporum*	24
CAA76703	*Gibberella fujikuroi*	23
CAB56503	*Catharanthus roseus*	14
AAB94588	*Glycine max*	14
CAA91268	*Caenorhabditis elegans*	12

Figure 7 – Amino acid homology alignment of A. ochraceus and human oxidoreductase to NADPH cytochrome P450 reductases from A. niger, mouse, and S. cerevisiae

```
PMON45605   1   MGDSHVDTSSTVSEAVAEEVSLFSMTDMELFSLIVGLLTYWFLFRKKKEEMPEFTKIQTL
human       1   MGDSHVDTSSTVSEAVAEEVSLFSMTDMELFSLIVGLLTYWFLFRKKKEEVPEFTKIQTL
mouse       1   MGDSHEDTSATVPEAVAEEVSLFSTTDIVLFSLIVGVLTYWFIFKKKKEEIPEFSKIQTT
pMON45632   1   --MAQLDTLDLVVLVALLVGSVAYFTKG---------TYWAVAKDYA--SAGPAMTGG
niger       1   --MAQLDTLDLVVLAVLLVGSVAYFIKG---------TYWAVAKTEMP--LPAPRMNGA
yeast       1   -MPFGIDNTDFTVLAGLVLAVLLLYVKRN---------SIKBLLMSDDG-------DIT-

PMON45605   61  TSSVRESSFVEKMRKTGRNIIVFYGSQTGTAEEFANRLSKD-AHRYGMRGMSADPEEYDL
human       61  TSSVRESSFVEKMRKTGRNIIVFYGSQTGTAEEFANRLSKD-AHRYGMRGMSADPEEYDL
mouse       61  APPVKESSFVEKMRKTGRNIIVFYGSQTGTAEEFANRLSKD-AHRYGMRGMSADPEEYDL
pMON45632   47  AKAGKTRDIVQKMDETGKNCVTFYGSQTGTAEDYASRLKEGSQRFGLKTMVADLEDYDY
niger       47  AKAGKTRNILEKMEETGKNCVTFYGSQTGTAEDYASRLAKEGSQRFGLKTMVADLEEYDY
yeast       42  AVSSGNRDIACVVTENNFNYLVLYASQTGTAEDYAKKFSKELVAKFNLNVMCADVENYDF

PMON45605   120 ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWLQ------ET-----DVDLSGVKF
human       120 ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWLQ------ET-----DVDLSGVKF
mouse       120 ADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQ------ET-----DVDLTGVKF
pMON45632   107 ENLEKFPE-DK-VMFFVLATYGEGEPTDNAMEFYQFVTGEDAAFESGATADDKFLSSLKY
niger       107 ENLDQFPE-DK-VAFFVLATYGEGEPTDNAMEFYQFFTGDDVAFES-ASADEKPLSKLKY
yeast       102 ESLNDVEV----IVSIFISTYGEGDFFLGAVNFEDFICN----ABAG------ALSNLRT

PMON45605   169 AVFGLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDL-DGNLEEDFITWREQFWPAV
human       169 AVFGLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGDD-DGNLEEDFITWREQFWPAV
mouse       169 AVFGLGNKTYEHFNAMGKYVDQRLEQLGAQRIFELGLGDL-DGNLEEDFITWREQFWPAV
pMON45632   165 VTFGLGNNTYEHYNAMVPNVDAALTKFGAQRIGSAGEGDDGAGTMEEDFLAWKSPMAAAL
niger       164 VAFGLGNNTYEHENAMVEQVIAAFGKLGFQRIGSAGEGDDGAGTMEEDFIAWKRPMAAAL
yeast       148 NFGLGNSTYPFFNGAAKKAEKHLSAAGAIRLGKLGEADDGACTTDEDYMAWKLSILEVL

PMON45605   228 CEHFGVEATGEESSIRQYELVVHTD----IDAAKVYMGEMGRLKSY---------BNQKP
human       228 CEHFGVEATGEESSIRQYELVVHTD----IDAAKVYMGEMGRLKSY---------BNQKP
mouse       228 CEFFGVEATGEESSIRQYELVVHED----MDTAKVYTGEMGRLKSY---------BNQKP
pMON45632   225 SEAMNLG----ERDAVYEPVFNVTEDESLSPEDENVYLGEPTQGHLQ---------GEPNG
niger       224 SESMDLE----EREAVYEPVFCVTENESLSPEDETVYLGEPTQSHLQ---------GTPNG
yeast       208 KLELHLD----EQEAKFTSCFQYTVLN---EITDSMSLGEPSAHYLPSHQLNRNADGIQLG

PMON45605   275 PFDAKNPFLAAVTTNRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQL
human       275 PFDAKNPFLAAVTTNRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQL
mouse       275 PFDAKNPFLAAVTTNRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSTLVNQI
pMON45632   273 PVSAHNPFLAPISESRELFNVKDRNCLHMETSIRGSNLTYQTGDHIAVWPTNAGSEVDRF
niger       272 PVSAHNPFLAPIAESRELFTVKDRNCLHMEISIPGSNLSYQTGDHIAVWPTNAGAEVTRF
yeast       262 PFDLSQPYIAPIVKSRELFSSNDRNCIHSEFDLSGSNIKYSTGDHIAVWPSNPLEKVEQF

PMON45605   335 GKILGAD--LDVVMSLNNLDEESNKKHPFICPTSYRTALTYYLDITNPPRTNVLYELAQY
human       335 GKILGAD--LDVVMSLNNLDEESNKKHPFPCPTSYRTALTYYLDITNPPRTNVLYELAQY
mouse       335 GEILGAD--LDVIMSLNNLDEESNKKHPFPCPTTYRTALTYYLDITNPPRTNVLYELAQY
pMON45632   333 LQAFGLEGKRHSVINIKGID---VTAKVEIPTPTTYDAAIRYYLEVCAEVSRCFVSTLAAF
niger       332 LQVFGLEGKRDSVLNIKGLD---VTAKVEIPTPTTYDAAVRYYLEVCAEVSRCFVATLAAF
yeast       322 LSIFNLD--PETIFDLKPLD---PTVKVPFPTPTTIGAALKYYLEITGFGEVSRQLFSSLIQF

PMON45605   393 AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
human       393 AS-EPSEQELLRKMASSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
mouse       393 AS-EPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYP-SLRPPIDHLCELLPR
pMON45632   391 APDEATKAEIVRLGGDKDYFHEKITNRCFNIAQ--ALQSITSKP-FTAVPFSLLIEGITK
niger       390 APMRKARQRLCVWAQG-LFPREGHQPMLQHAQ--ALQSITSKP-FSAVPFSLLIEGITK
yeast       378 APNADVKEKLTLLSKDKDQFAVEITSKGFNIAD--ALKYLSDGAKWDNVPLQFLVESVEQ

PMON45605   451 LQARYYSIASSSKVHPNSVHICAVVVEYETK----AGRINKGVATNWLRAKEP---AGE--
human       451 LQARYYSIASSSKVHPNSVHICAVVVEYETK----AGRINKGVATNWLRAKEP---AGE--
mouse       451 LQARYYSIASSSKVHPNSVHICAVAVEYEAK----SGRVNKGVATSWLRTKEP---AGE--
pMON45632   448 LQPRYYSISSSSLVQKDKISITAVVESVRLP---GEEHIVKGVTTNYLLALKEKQGEPS
niger       446 LQPRYYSISSSSLVQKEKISITAVVESVRLP---GASHVVKGVTTNYLLALKQKQNGRSL
yeast       436 MTPRYYSISSSSLSEKQTVHVTSIVENFPNPELP-DAPPGVGVTTNLLRNIQLAQNNVNI
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← Insert

"Figure 7, Continued"

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        PMON45605   503 -----------NCGF-----ALVPFFVRKSQFRLPFRATTPVIMVGPGTGVAPFIGFIQE
        human       503 -----------NCGF-----ALVPFFVRKSQFRLPFRATTPVIMVGPGTGVAPFIGFIQE
        mouse       503 -----------NCRF-----ALVPFFVRKSQFRLPFKPFTPVIMVGPGTGVAPFLGFIQE
        pMON45632   505 PDPHG-LTYSITGPRNKYDGIHVPVHVRHSNFKLFSDPSRPVIMVGPGTGVAPFRGFIQE
 5      niger       503 SRPSR-LDLLHHGPRNKYDGIHVPVHVRHSNFKLFSDPSRELIIMVGPGTGVAPFRGFIQE
        yeast       495 AETNLPVHYDLNGPRKLFANYKLPVHVRRSNFRLPSNPSTPVIMIGPGTGVAPFRGFIRE


        PMON45605   547 RAWLRQ---QGKE---VGETLLYYGCRRSDEDYLYREELAQFHRL-GALTQLNVAFSRE-
10      human       547 RAWLRQ---QGKE---VGETLLYYGCRRSDEDYLYREELAQFHRL-GALTQLNVAFSRE-
        mouse       547 RAWLRE---QGKE---VGETLLYYGCRRSDEDYLYREELARFHKL-GALTQLNVAFSRE-
        pMON45632   564 RAALAA---KGEK---VGTTLLFFGCRZSDEDFLYKDEWKTFQEQLGDSLKIITAFSRE-
        niger       562 RAALAA---KGEK---VGPTVLFFGCRKSDEDFLYKDEWKTYQDQLGDNLKIITAFSRE-
        yeast       555 RVAFLESQKKGNNVSLGKHILFYGSRNTL-DFLYQDEWPEYAKKLDGSFEMVVAHSFLP
15

        PMON45605   599 QSHKVYVQHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQ
        human       599 QSHKVYVQHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQ
        mouse       599 QAHKVYVQHLLKRDKEHLWKLIHEGGAHIYVCGDARNMAZDVQNTFYDIVAEFGFMEHTQ
20      pMON45632   617 SAEKVYVQHRLRDHAELVSDLI-KQKATFYVCGDAANMAREVNLVLGQITAKQRGLPAEK
        niger       615 GPQKVYVQHRLRDHSELVSDLI-KQKATFYVCGDAANMAREVNLVLGQITAAQRGLPAEK
        yeast       614 NTKKVYVQDKLKLYEDQVFEMI-NNGAFIYVCGDAKGMAFGVSTALVGILSRGKSITTDE

25      PMON45605   658 AVDYIKKLMTKGRYSLDVWS
        human       658 AVDYIKKLMTKGRYSLDVWS
        mouse       659 AVDYVKKLMTKGRYSLDVWS
        pMON45632   676 GEDMVKHMRSSGSYQDDVWS
30      niger       674 GEDMVKHMRRGRYQBDVWS
        yeast       673 ATELIKMLKTSGRYQBDVW-

        PMON45605       (SEQ ID NO: 03)
        human           (SEQ ID NO: 06)
        mouse           (SEQ ID NO: 39)
35      PMON45632       (SEQ ID NO: 05)
        niger           (SEQ ID NO: 38)
        yeast           (SEQ ID NO: 37)
```

Figure 8 – Amino acid homology alignment of A. ochraceus oxidoreductase to NADPH cytochrome P450 reductases from A. niger and S. cerevisiae

```
A.niger       1  -MAQLDTLDLVVLAVLLVGSVAYFTKGTYWAVAKTRMPLPAFRMNGAAKAGKTRNIIEKM
A.ochraceus   1  -MAQLDTLDLVVLVALLVGSVAYFTKGTYWAVAKDPYPSAGEAMNGGAKAGKTRDIVQKM
S.cerevisiae  1  MPFGIDNTPFTVLAGLVLAVILYVKRNSIKELLMSDDCDITAVSSC------NRDIAGVV

A.niger      60  EETGKNCVIFYGSQTGTAEDYASRLAKEGSQRFGLKTMVADLEEYDYENLIQFPEDKVAF
A.ochraceus  60  DETGKNCVIFYGSQTGTAEDYASRLAKEGSQRFGLKTMVADLEDYDYENLEKFPEDKVVF
S.cerevisiae 55  TENNKNYLVLYASQTGTAEDYAKKFSKELVAKRNLNVMCADVENYDFESLNDVP--VIVS

A.niger     120  FVLATYGEGEPTDNAVEFYQFLTGDDVAFES-ASADEKPLSKLKYVAFGLGNNTYEHYNA
A.ochraceus 120  FVLATYGEGEPTDNAVEFYQFVTGEDAAFESGATADDKPLSSLKYVIFGLGNNTYEHYNA
S.cerevisiae 113 IFISTYGEGDFPDGAVNFEDFIC---------NABAGALSNLRYNMFGLGNSTYEFFNG

A.niger     179  MVRQVDAAFQRLGEQRIGSAGEGDDGAGTMEEDFLAWKEPMWAALSPSMDLEEREAVYEF
A.ochraceus 180  MVRNVDAALTKFGAQRIGSAGEGDDGAGTMEEDFLAWKEPMWAALSPAMNLQERDAVYEF
S.cerevisiae 163 AAKKAEKHLSAAGAIRLGKLGEADDGAGTTDEDVMAWKDSILEVLKLEIHLDEQEAKFTS

A.niger     239  VFQVTENESLSPEDEIVYLGEPTQSHLQ---------GTPKGPYSAHNPFIAPIAESREL
A.ochraceus 240  VFNVTEDESLSPEDNVVYLGEPTQGHLQ---------GEPKGPYSAHNPFIAPISESREL
S.cerevisiae 223 QFCYT---VLNEITDSMSLGEPSAHYLPSHQLNRNADCIQLGPFDLSQPVIAPIVKSREL

A.niger     290  FIIVKDRNCLHMEISIAGSNLSYQTGDHIAVWPTNACAEVDRFLQVFGLEGKRDSVINIKG
A.ochraceus 291  FNVKDRNCLHMEISIAGSNLTYQTGDHIAVWPTNAGSEVDRFLQAFGLEGKRHSVINIKG
S.cerevisiae 280  FSSNDRNCIHSEFDLSGSNIKYSTGDHIAVWPSNPLEKVEQFLSIFNLEP--ETIFDLKP

A.niger     350  IDVTAKVPIPTPTTYDAAVRYYMEVCAPVSRQFVATLAAFAEMRKARQRLQVWVAQG-LF
A.ochraceus 351  IDVTAKVPIPTPTTYDAAVRYYLEVCAPVSRQFVSTLAAFAEDEATRAEIVRLGGDKDYF
S.cerevisiae 338  ILPTVKVFPTPTTIGAAIKHYLEITGPVSRQLFSSLIQFAENADVRKFKLTLLSKDKDQF

A.niger     409  PREGHCPMLQHAQALQSITS-KPFSAVPFSLLIEGITKLQPRYYSISSSSLVQKDKISIT
A.ochraceus 411  HEKITNRCFNIAQALQSITS-KPFTAVPFSLLIEGITKLQPRYYSISSSSLVQKDKISIT
S.cerevisiae 398  AVEITSNYFNIADALKYLSDGAKEDNVEMQFLVESSPQMTPRYYSISSSLSEKQTVHVI

A.niger     468  AVVESVRLE--CASHMVKGVTTNYLLALKQKQNGRSLSRESR-LDLLHHGPRNKYDGIHV
A.ochraceus 470  AVVESVRLE--GEPHIVKGVTTNYLLALREKQNGEPSPDEHG-LTYSITGPRNKYDGIHV
S.cerevisiae 458  SIVENFPNEELPDAPPGVGVTTNLLRNIQLAQNNVNIAETNLPVHYDLNGPRKLEANYKL

A.niger     525  PVHVRHSNFKLPSDPSRPIIIMVGPGTGVAPFRGFIQERAALAAKGEK------VGPTVLF
A.ochraceus 527  PVHVRHSNFKLPSDPSRPVIMVGPGTGVAPFRGFIQERAALAAKGEK------VGTTVLF
S.cerevisiae 518  PVHVRRSNFRLPSNPSTPVIMTGPGTGVAPFRGFIRERVAFLESQKKGGNNVSLGKHILF

A.niger     579  FGCRKSDEDFLYKDEWKTYQDQLGDNLKIITAFSRE-GPQKVYVQHRLREHSELVSDLLK
A.ochraceus 581  FGCRKSDEDFLYKDEWKTRQEQLGDSLKIITAFSRE-SAEKVYVQHRLREHAELVSDLLK
S.cerevisiae 578  YGSRNTD-DFLYQDEWPEYAKKLDGSFEMVVAHSRLPNTKKVYVQDRLKEYBIQVFEMIN

A.niger     638  QKATFYVCGDAANMAREVNLVLGQIIAAQRGLPAEKGEEMVKHMRRGRYQEDVWS
A.ochraceus 640  QKATFYVCGDAANMAREVNLVLGQIIARQRGLPAEKGEEMVKHMRSSGSYQDDVWS
S.cerevisiae 637  NGAFIYVCGDAKGMAKGVSTALVGILSRGFSITTDEATELIKMLKTSGRYQEDVW-
```

```
A.ochraceus,  PMON45632   (SEQ ID NO: 05)
A.niger                   (SEQ ID NO: 38)
S.cerevisiae, yeast       (SEQ ID NO: 37)
```

Replacement Sheet

Figure 9 – Phylogenetic tree showing the relatedness of
Aspergillus ochraceus and *human oxidoreductase to*
reductases from A. niger, *yeast, and mouse.*

PMON45605

human

pMON45632

niger

yeast

mouse

5
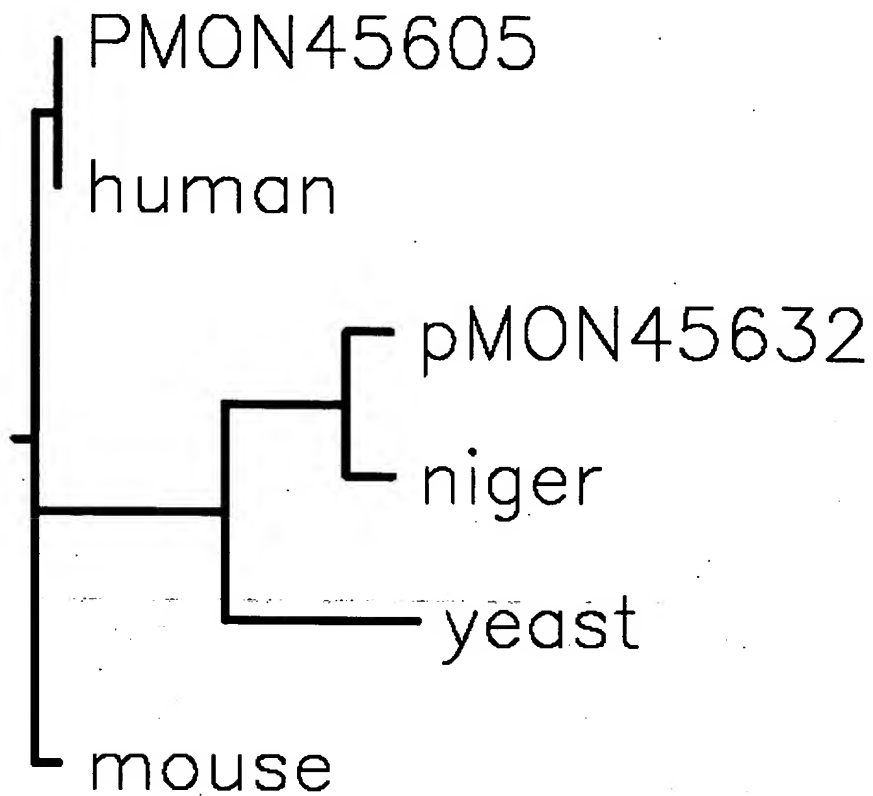
S03196-00-US

Figure 10 – Percent homology between Aspergillus ochraceus oxidoreductase to reductases from A. niger, yeast, and mouse and human.

Accession number	organism	% id to A.och oxred
CAA81550	A. niger	84
BAA02936	S. cerevisiae	37
BAA04496	mouse	34
AAB21814	human	33

Replacement Sheet

Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

```
PMON45605    1  MGDSHVDTSSTVSEAVAEEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFTKIQTL
human        1  MGDSHVDTSSTVSEAVAEEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFTKIQTL
rabbit       1  MADSHGDTCATLPEAAAQEASVFSMTDVVLFSLIVGLITYWFLFRKKKEEVPEFTKICAP
rat          1  MGDSHPDTSATVPEAVAEEVSLFSTTDMVLFSLIVGVLTYWFIFRKKKEEIPEFSKIQTT
mouse        1  MGDSHPDTSATVPEAVAEEVSLFSTTDIVLFSLIVGVLTYWFIFRKKKEEIPEFSKIQTT
pig          1  MGDSNVDTGTITSEMVAEEVSLFSATDMVLFSLIVGLLTYWFIFRKKKDEVPEFSKIETT


PMON45605   61  TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDL
human       61  TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDL
rabbit      61  TSSSVKESSFVEKMKKTGRNIVVFYGSQTGTAEEFANRLSKDAHRYGMRGMAADPEEYDL
rat         61  APP-VKESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDL
mouse       61  APP-VKESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDL
pig         61  TSS-VKDSSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMAADPEEYDL


PMON45605  120  ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWLQETDVDLSGVKFAVFGLGNKTYE
human      120  ADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWLQETDVDLSGVKFAVFGLGNKTYE
rabbit     121  ADLSSLPEINNALAVFCMATYGEGDPTDNAQDFYDWLQETDVDLSGVKFAVFGLGNKTYE
rat        120  ADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQETDVDLTGVKFAVFGLGNKTYE
mouse      120  ADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQETDVDLTGVKFAVFGLGNKTYE
pig        120  SDLSSLPEIENALAVFCMATYGEGDPTDNAQDFYDWLQEADVDLTGVKYAVFGLGNKTYE


PMON45605  180  HFNAMGKYVDKRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
human      180  HFNAMGKYVDKRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHFGVEATGEE
rabbit     181  HFNAMGKYVDQRLEQLGAQRIFELGMGDDDANLEEDFITWREQFWPAVCEHFGVEATGEE
rat        180  HFNAMGKYVDQRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEFFGVEATGEE
mouse      180  HFNAMGKYVDQRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEFFGVEATGEE
pig        180  HFNAMGKYVDKRLEQLGAQRIFDLGLGDDDGNLEEDFITWREQFWPAVCEHFGVEATGEE


PMON45605  240  SSIRQYELVVHTDIDAAKVYMGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
human      240  SSIRQYELVVHTDIDAAKVYMGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
rabbit     241  SSIRQYELVLHTDIDVAKVYQGEMGRLKSYENQKPPFDAKNPFLTVTTNRKLNQGTERH
rat        240  SSIRQYELVVHFDMDVAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTERH
mouse      240  SSIRQYELVVHFDMDTAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTTNRKLNQGTERH
pig        240  SSIRQYELVVHTDMDTAVVYTGEMGRLKSYENQKPPFDAKNPFLAVVTTNRKLNQGTERH


PMON45605  300  LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGKILGADLDVVMSLNNLDEESNKKH
human      300  LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGKILGADLDVVMSLNNLDEESNKKH
rabbit     301  LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGADLDVVMSLNNLDEESNKKH
rat        300  LMHLELDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKH
mouse      300  LMHLELDISDSKIRYESGDHVAVYPANDSTLVNQIGEILGADLDVIMSLNNLDEESNKKH
pig        300  LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGTDLDIVMSLNNLDEESNKRH


PMON45605  360  PFPCPTSYRTALTYYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
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Replacement Sheet

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"Figure 11, continued"

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        human   360 PFPCPTSYRTALTYYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
        rabbit  361 PFPCPTSYRTALTYYLDITNPPRTNVLYELAQYAADPAEQEQLRKMASSSGEGKELYLSW
        rat     360 PFPCPTIYRTALTYYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSW
        mouse   360 PFPCPTIYRTALTYYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSW
5       pig     360 PFPCPTIYRTALTYYLDITNPPRTNVLYELAQYASEPSEQEQLRKMASSSGEGKELYLSW


        PMON45605 420 VVEARRHILAILQDCPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
        human   420 VVEARRHILAILQDCPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
10      rabbit  421 VVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYE
        rat     420 VVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYE
        mouse   420 VVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYE
        pig     420 VVEARRHILAILQDYPSLRPPIDHLCBRLPRLQARYYSIASSSKVHPNSVHICAVVVEYE


15
        PMON45605 480 TKAGRIINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAF
        human   480 TKAGRIINKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAF
        rabbit  481 TKAGRIINKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAF
        rat     480 AKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKSTTPVIMVGPGTGIAF
20      mouse   480 AKSGRVNKGVATSWLRTKEPAGENGRRALVPMFVRKSQFRLPFKFTTPVIMVGPGTGVAF
        pig     480 TKSGRVNKGVATSWLRAKEPAGENGRRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVAF
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"Figure 4, continued"

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PMON45605   540  FIGFIQERAWLRQQGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGALTQLNVAFSREQ
human       540  FIGFIQERAWLRQQGKEVGETLLYYGCRRSDEDYLYREELAQFHRDGALTQLNVAFSREQ
rabbit      541  FIGFIQERAWLRQQGKEVGETLLYYGCRRAAEDYLYREELAGFQKDGTLGQLNVAFSREQ
rat         540  FMGFIQERAWLRBQGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQ
mouse       540  FMGFIQERAWLRPQGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQ
pig         540  FIGFIQERAWLQBQGKEVGETLLYYGCRRSDEDYLYREELAQFHAKGALTRLSVAFSREQ


PMON45605   600  SHKVYVQHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
human       600  SHKVYVQHLLKQDREHLWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
rabbit      601  AQKVYVQHLLRRDKEHLWRLIHEGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQA
rat         600  AHKVYVQHLLKRDREHLWKLIHEGGAHIYVCGDARNMAKDVQNTFYDIVABFGFMEHTQA
mouse       600  AHKVYVQHLLKRDKEHLWKLIHEGGAHIYVCGDARNMAKDVQNTFYDIVABFGFMEHTQA
pig         600  PQKVYVQHLLKRDKEHLWKLIHDGGAHIYICGDARNMARDVQNTFCDIVAEQGFMEHAQA


PMON45605   659  VDYIKKLMTKGRYSLDVWS      (SEQ ID NO: 03)
human       659  VDYIKKLMTKGRYSLDVWS      (SEQ ID NO: 52)
rabbit      661  VDYVKKLMTKGRYSLDVWS      (SEQ ID NO: 53)
rat         660  VDYVKKLMTKGRYSLDVWS      (SEQ ID NO: 54)
mouse       660  VDYVKKLMTKGRYSLDVWS      (SEQ ID NO: 55)
pig         660  VDYVKKLMTKGRYSLDVWS      (SEQ ID NO: 56)
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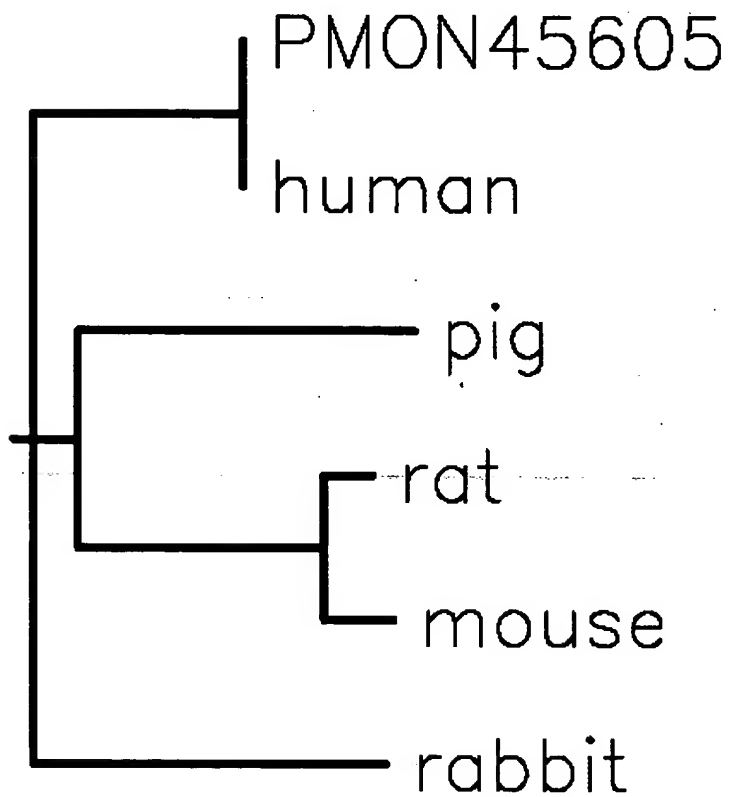
Figure 12 — Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt

5

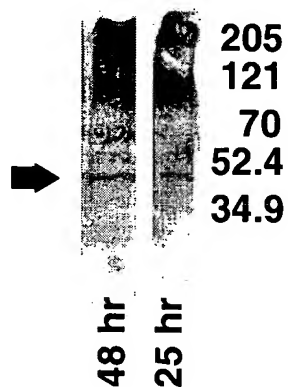**Figure 13 – Percent homology between human oxidoreductase and top 4 hits from SwissProt**

Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

Figure 14 · Expression of Aspergillus ochraceus 11 alpha hydroxylase in transfected Sf9 insect cells

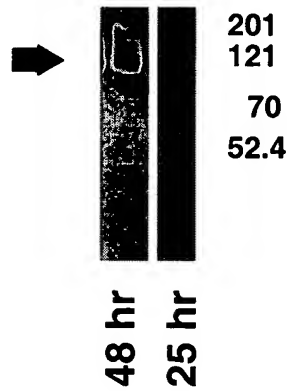## Expression of 11-α-Hydroxylase in Transfected Sf9 Cells

Figure 15 - Expression of Aspergillus ochraceus *P450*

oxidoreductase in transfected Sf9 insect cells

Expression of Fungal P-450 Oxidoreductase
in Transfected Sf9 Cells

Replacement Sheet

Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

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